TOPIC 4

DNA, genes, chromosomes and protein synthesis

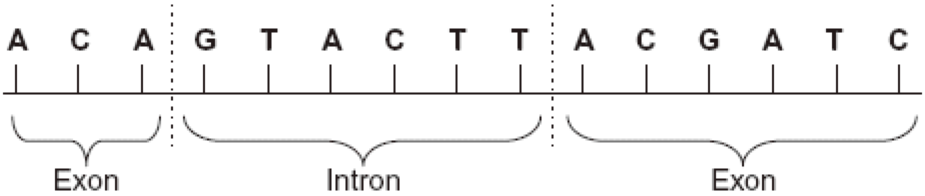
Pack 2

Q12. (a) Complete the table to show the differences between DNA, mRNA and tRNA.

Type of nucleic acid	**Hydrogen bonds present (✓) or not present (✗)**	**Number of polynucleotide strands in molecule**
DNA	✓	2
mRNA	✗	1
tRNA	✓	1

(2)

(b) The diagram shows the bases on one strand of a piece of DNA.



(i) In the space below, give the sequence of bases on the pre-mRNA transcribed from this strand.

U G U C A U G A A U G C U A G

(2)

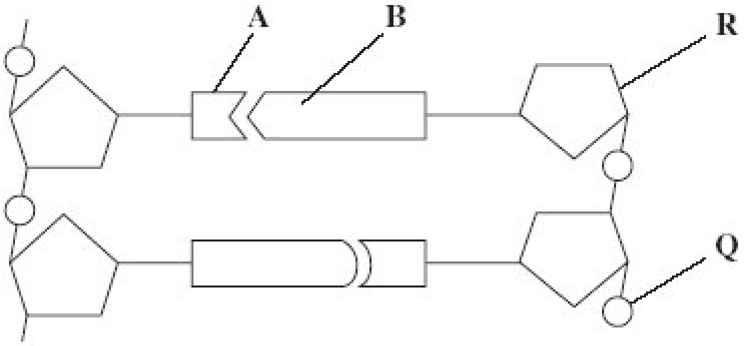
(ii) In the space below, give the sequence of bases on the mRNA produced by splicing this piece of pre-mRNA.

U G U U G C U A G

(1)
(Total 5 marks)

Q13. **Figure 1** shows a short section of a DNA molecule.

Figure 1



(a) Name parts **R** and **Q**.

(i) **R** Deoxyribose sugar ....

(ii) **Q** Phosphate ....

(2)

(b) Name the bonds that join **A** and **B**.

Hydrogen bonds ....

(1)

(c) Ribonuclease is an enzyme. It is 127 amino acids long.

What is the minimum number of DNA bases needed to code for ribonuclease?

381

(1)

(d) **Figure 2** shows the sequence of DNA bases coding for seven amino acids in the enzyme ribonuclease.

Figure 2

G T T T A C T A C T C T T C T T C T T T A

The number of each type of amino acid coded for by this sequence of DNA bases is shown in the table.

Amino acid	Number present
Arg	3
Met	2
Gln	1
Asn	1

Use the table and **Figure 2** to work out the sequence of amino acids in this part of the enzyme. Write your answer in the boxes below.

Gln	Met	Met	Arg	Arg	Arg	Asn

(1)

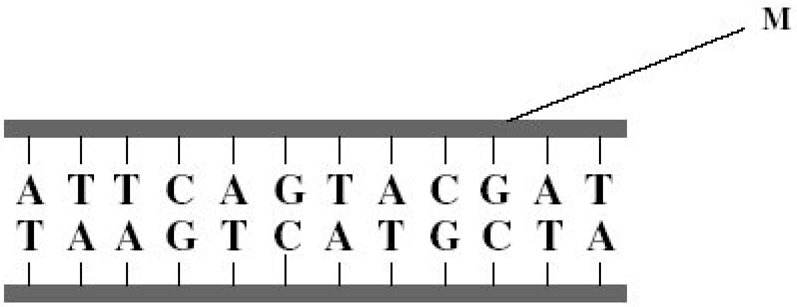
(e) Explain how a change in a sequence of DNA bases could result in a non-functional enzyme.

A change in sequence of DNA bases causes a change in the sequence of amino acids. This causes the hydrogen, ionic, and disulfide bonds to change, making the tertiary structure different.

This change means the substrate can no longer bind to the active site

(3)
(Total 8 marks)

Q14. The diagram shows part of a DNA molecule.



(a) Name the **two** components of the part of the DNA molecule labelled **M**.

1 Phosphate group

2 Deoxyribose sugar

(2)

(b) What is the maximum number of amino acids for which this piece of DNA could code?

4

(1)

(c) Scientists calculated the percentage of different bases in the DNA from a species of bacterium. They found that 14% of the bases were guanine.

(i) What percentage of the bases in this species of bacterium was cytosine?

Answer 14%

(1)

(ii) What percentage of the bases in this species of bacterium was adenine?

Answer 36%

(1)

(d) The scientists found that, in a second species of bacterium, 29% of the bases were guanine.

Explain the difference in the percentage of guanine bases in the two species of bacterium.

The different bacteria have different genes, which causes a different DNA

base sequence

(2)
(Total 7 marks)

Q15. The table shows the sequence of bases on part of the coding strand of DNA.

Base sequence on coding strand of DNA	**C**	**G**	**T**	**T**	**A**	**C**
Base sequence of mRNA	G	C	A	A	U	G

(a) Complete the table to show the base sequence of the mRNA transcribed from this DNA strand.

(2)

(b) A piece of mRNA is 660 nucleotides long but the DNA coding strand from which it was transcribed is 870 nucleotides long.

(i) Explain this difference in the number of nucleotides.

Introns are present in DNA, which are removed

(1)

(ii) What is the maximum number of amino acids in the protein translated from this piece of mRNA? Explain your answer.

Number of amino acids 220

Explanation Three bases code for each amino acid ....

....

(2)

(c) Complete the table to give **two** differences between the structure of mRNA and the structure of tRNA.

mRNA	**tRNA**
No base pairing	Base pairing
mRNA is linear	tRNA is clover-leaf shaped

(2)
(Total 7 marks)

Q16. (a) The table shows the mRNA codons for some amino acids.

Codon	**Amino acid**
CUA	Leucine
GUC	Valine
ACG	Threonine
UGC	Cysteine
GCU	Alanine
AGU	Serine

(i) Give the DNA sequence coding for cysteine.

ACG

(1)

(ii) Name the amino acid coded by the tRNA anticodon UCA.

Serine

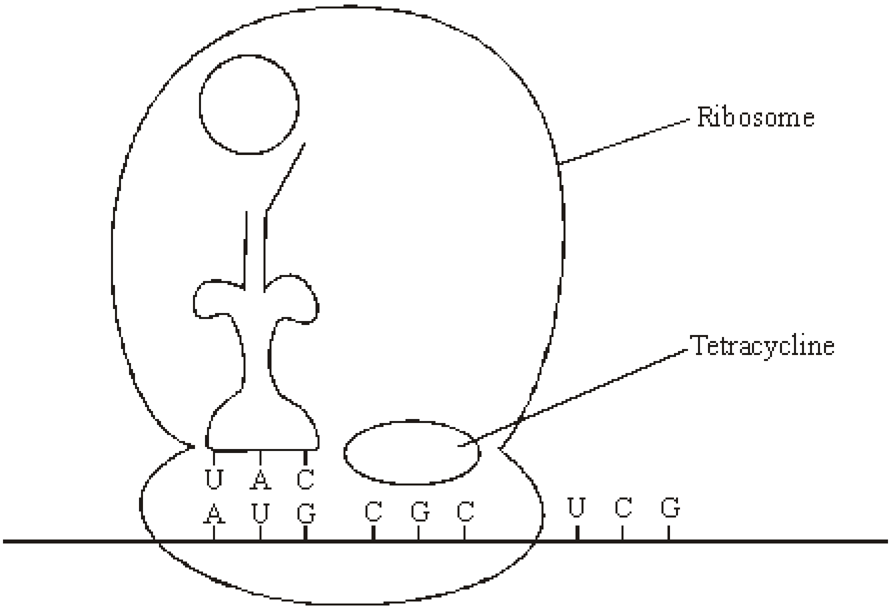
(1)

(b) A particular gene is 562 base-pairs long. However, the resulting mRNA is only 441 nucleotides long. Explain this difference.

DNA contains introns, which are edited out

(1)

(c) Tetracycline binds to bacterial ribosomes. This is shown in the diagram.



Protein synthesis in bacteria is similar to that in eukaryotic cells. Explain how tetracycline stops protein synthesis.

Tetracycline binds to the codon on mRNA, preventing the tRNA molecule

from being able to bind to it

....

(2)
(Total 5 marks)

Q17. Read the following passage.

> The sequence of bases in a molecule of DNA codes for proteins. Different sequences of bases
> code for different proteins. The genetic code, however, is degenerate. Although the base
> sequence AGT codes for serine, other sequences may also code for this same amino acid.
> There are four base sequences which code for the amino acid glycine. These are CCA, CCC,
> CCG and CCT. There are also four base sequences coding for the amino acid proline. These
> are GGA, GGC, GGG and GGT.
>
> Pieces of DNA which have a sequence where the same base is repeated many times are called
> “slippery”. When “slippery” DNA is copied during replication, errors may occur in copying.
> Individual bases may be copied more than once. This may give rise to differences in the
> protein which is produced by the piece of DNA containing the errors.

Use information in the passage and your own knowledge to answer the following questions.

(a) Different sequences of bases code for different proteins (lines 1 – 2). Explain how.

Proteins are made of chains of amino acids.
....

Each amino acid is coded for by its' own triplet code
....

....

....

(2)

(b) The base sequence AGT codes for serine (lines 2 – 3). Give the mRNA codon transcribed from this base sequence.

UCA
....

(2)

(c) Glycine-proline-proline is a series of amino acids found in a particular protein. Give the sequence of DNA bases for these three amino acids which contains the longest "slippery" sequence.

CCG

(2)

(d) (i) Explain how copying bases more than once may give rise to a difference in the protein (lines 9 – 10).

Changes is the DNA base sequence cause the amino acid chain to

be different, potentially forming a non-functional protein

(2)

(ii) At what stage in the cell cycle would these errors in copying DNA bases occur?

Interphase

(1)

(e) Starting with mRNA in the nucleus of a cell, describe how a molecule of protein is synthesised.

mRNA leaves the nucleus through a nuclear pore, to a ribosome.

tRNA molecules bring amino acids to the ribosomes, with complementary anti-codons binding to the mRNA molecule. Peptide bonds are formed between amino acids.

tRNA molecules detach from the mRNA molecule and polypeptide chain, collecting another amino acid. The ribosome moves along the mRNA molecule, forming th entire polypeptide chain

....

....

....

....

(6)
(Total 15 marks)

Q18. (a) **Table 1** shows some of the events which take place in protein synthesis.

A	tRNA molecules bring specific amino acids to the mRNA molecule
B	mRNA nucleotides join with exposed DNA bases and form a molecule of mRNA
C	The two strands of a DNA molecule separate
D	Peptide bonds form between the amino acids
E	The mRNA molecule leaves the nucleus
F	A ribosome attaches to the mRNA molecule

Table 1

(i) Write the letters in the correct order to show the sequence of events during protein synthesis, starting with the earliest.

C B E F A D

(2)

(ii) In which part of a cell does **C** take place?

Nucleus

(1)

(iii) Which of **A - F** are involved in translation?

A, D, F

(1)

(b) **Table 2** shows some mRNA codons and the amino acids for which they code.

mRNA codon	**Amino acid**
GUU	Valine
CUU	Leucine
GCC	Alanine
AUU	Isoleucine
ACC	Threonine

Table 2

(i) A tRNA molecule has the anticodon UAA. Which amino acid does the tRNA molecule carry?

Isoleucine

(1)

(ii) Give the DNA base sequence that codes for threonine.

TGG

(1)
(Total 6 marks)

Q19. (a) (i) What is the role of RNA polymerase in transcription?

Attaches nucleotides to the backbone

Forms phosphodiester bonds

(1)

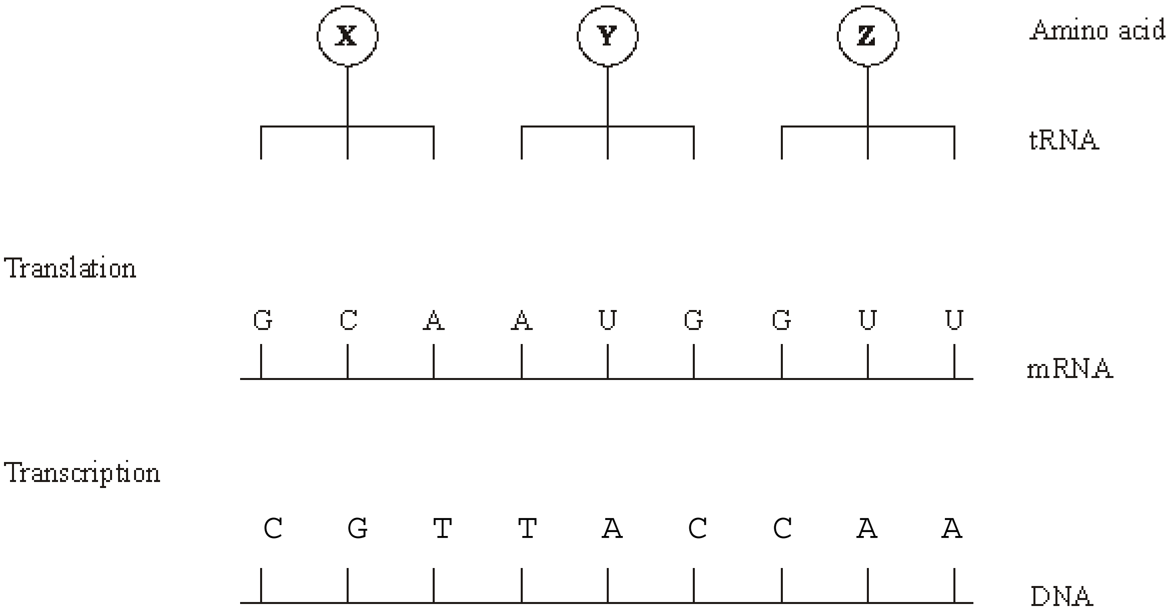
(ii) Name the organelle involved in translation.

Ribosomes

(1)

(b) **Figure 1** shows some molecules involved in protein synthesis.

Figure 1



Complete **Figure 1** to show

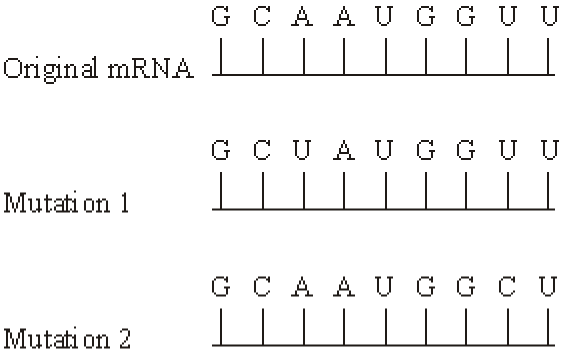
(i) the bases on the DNA strand from which the mRNA was transcribed;

(ii) the bases forming the anticodons of the tRNA molecules.

(2)

Figure 2 shows the effects of two different mutations of the DNA on the base sequence of the mRNA. The table shows the mRNA codons for three amino acids.

Figure 2



Amino acid	**mRNA codon**
methionine	AUG
valine	GUC GUU
alanine	GCA GCC GCU

(c) Name the type of mutation represented by mutation 1.

....

(1)

(d) Use the information in the table to

(i) identify amino acid **X** in **Figure 1**;

....

(1)

(ii) explain how each mutation may affect the polypeptide for which this section of DNA is part of the code.

Mutation 1 ....

....

....

....

(2)

Mutation 2 ....

....

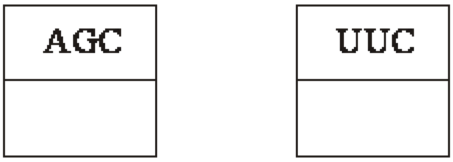
....

....

(2)
(Total 10 marks)

Q20. (a) **Figure 1** shows the exposed bases (anticodons) of two tRNA molecules involved in the synthesis of a protein.

Figure 1



Complete the boxes to show the sequence of bases found along the corresponding section of the coding DNA strand.

(2)

(b) Describe the role of tRNA in the process of translation.

....

....

....

....

....

....

(3)

(c) **Figure 2** shows the sequence of bases in a section of DNA coding for a polypeptide of seven amino acids.

Figure 2

TACAAGGTCGTCTTTGTCAAG

The polypeptide was hydrolysed. It contained four different amino acids. The number of each type obtained is shown in the table.

Amino acid	**Number present**
Phe	2
Met	1
Lys	1
Gln	3

Use the base sequence shown in **Figure 2** to work out the order of amino acids in the polypeptide. Write your answer in the table below.

Met						

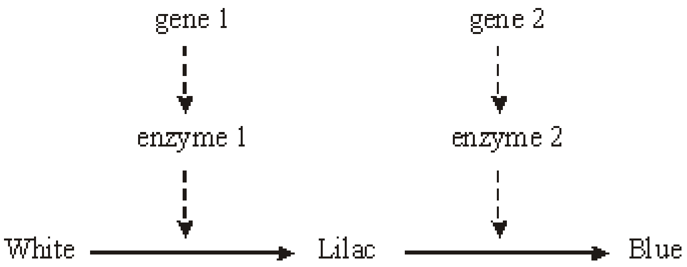
(2)
(Total 7 marks)

Q21. (a) Name **one** mutagenic agent.

....

(1)

(b) In flax plants the flowers are white, lilac or blue. The diagram shows the pathway by which the flower cells produce coloured pigments.



(i) A deletion mutation occurs in gene 1. Describe how a deletion mutation alters the structure of a gene.

....

....

....

....

(2)

(ii) Describe and explain how the altered gene could result in flax plants with white-coloured flowers.

....

....

....

....

....

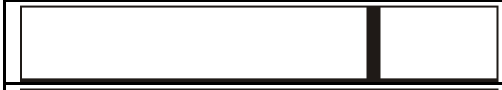
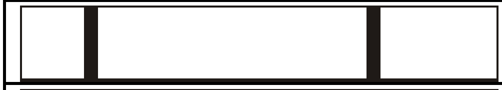
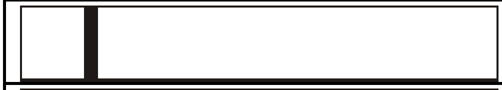
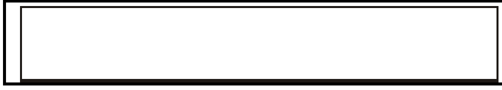
....

....

....

(4)

(iii) Electrophoresis was used to separate the enzymes involved in this pathway. When extracts of the differently coloured flax petals were analysed, four different patterns of bands were produced. In the table, only bands that contain functional enzymes are shown.

Result of electrophoresis	**Colour of petal**
	White
	
	
	

Complete the table to give the colour of the petal from which each extract was taken.

(2)
(Total 9 marks)

Q22. Lysozyme is an enzyme consisting of a single polypeptide chain of 129 amino acids.

(a) What is the minimum number of nucleotide bases needed to code for this enzyme?

....

(1)

(b) The diagram shows the sequence of bases in a section of the mRNA strand used to synthesise this enzyme.

G G U C U U U C U U A U G G U A G A U A
U

(i) Give the DNA sequence which would be complementary to the first four bases in this section of mRNA.

....

(1)

(ii) How many different types of tRNA molecule would attach to the section of mRNA shown in the diagram?

....

(1)

(c) Give **two** factors which might increase the frequency at which a mutation in DNA occurs.

1 ....

2 ....

(2)

(d) Two single base mutations occurred in the DNA coding for this section of mRNA. These mutations caused an alteration in the sequence of amino acids in the enzyme. The diagram shows the original and altered sequences of amino acids.

Original amino acid sequence	Gly	Leu	Ser	Tyr	Gly	Arg	Tyr
Original mRNA base sequence	GGU	CUU	UCU	UAU	GGU	AGA	UAU

Altered amino acid sequence	Gly	Leu	Tyr	Leu	Trp	Arg	Tyr
Altered mRNA base sequence	GGU	CUU				AGA	UAU

(i) Use the mRNA codons provided in the table to complete the altered mRNA base sequence in the diagram.

Amino acid	**mRNA codons which can be used**
Arg	AGA
Gly	GGU
Leu	CUU or UUA
Ser	UCU
Trp	UGG
Tyr	UAU or UAC

(1)

(ii) Use the information provided to determine the precise nature of the **two** single base mutations in the DNA.

....

....

....

....

....

....

(3)
(Total 9 marks)

Q23. (a) CFTR is a transmembrane regulator protein. Its molecules have 1480 amino acids. People with cystic fibrosis produce defective CFTR protein which is missing one amino acid from its structure.

(i) What is the minimum number of bases on DNA which would code for the normal CFTR protein? Explain your answer.

Number of bases ....

....

....

....

....

(2)

(ii) Which type of gene mutation produced the cystic fibrosis allele? Explain your answer.

....

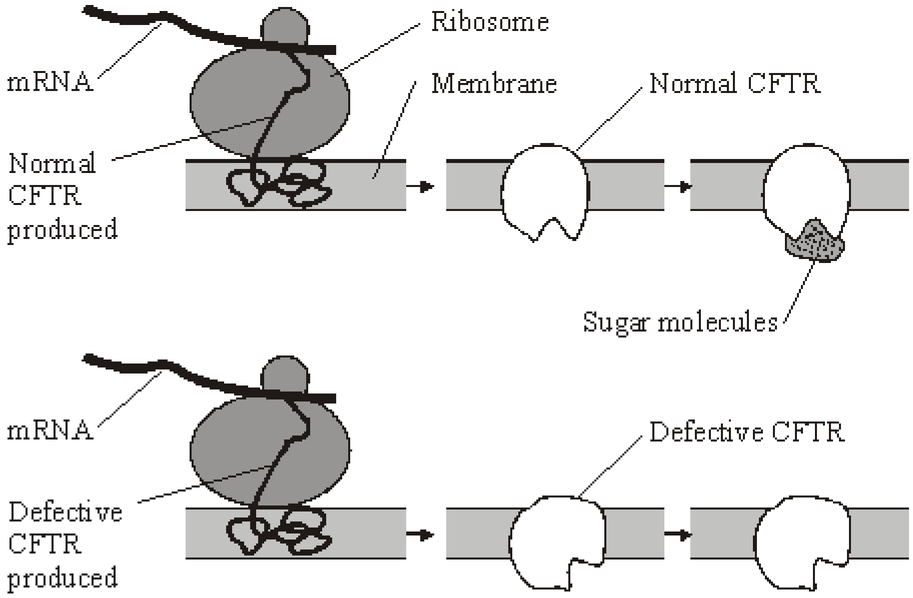
....

....

....

(2)

(b) The diagram shows part of the process of making normal and defective CFTR in a cell. A normal CFTR protein molecule has sugar molecules attached to it which make it functional.



(i) Describe how the information on mRNA is translated into CFTR at the ribosome.

....

....

....

....

....

....

....

....

(4)

(ii) Using information in the diagram and your own knowledge, suggest why defective CFTR, missing one amino acid, is not functional.

....

....

....

....

(2)

(Total 10 marks)

M12. (a)

DNA	✓	2
mRNA	✗	1
tRNA	✓	1

One mark for each correct column
Regard blank as incorrect in the context of this question
Accept numbers written out: two, one, one

2

(b) (i) Marking principles
1 mark for complete piece transcribed;

Correct answer
UGU CAU GAA UGC UAG

1 mark for complementary bases from sequence transcribed;

but allow 1 mark for complementary bases from section transcribed, providing all four bases are involved

2

(ii) Marking principle
1 mark for bases corresponding to exons taken from (b)(i)

Correct answer
UGU UGC UAG
If sequence is incorrect in (b)(i), award mark if section is from exons. Ignore gaps.

1

[5]

M13. (a) (i) Deoxyribose;

pentose / 5C sugar = neutral

1

(ii) Phosphate / Phosphoric acid;

phosphorus / P = neutral

1

(b) Hydrogen (bonds);

1

(c) 381 / 384 / 387;

1

(d) (Gln) Met Met Arg Arg Arg Asn;

1

(e) Change in (sequence of) amino acids / primary structure;

Change in hydrogen / ionic / disulfide bonds leads to change in tertiary structure / active site (of enzyme);

Substrate cannot bind / no enzyme-substrate complexes form;

Q Reject = different amino acids are formed

3

[8]

M14. (a) Phosphate;

Deoxyribose;

Q Candidates must specify deoxyribose. This term is a specification requirement.
Ignore anything that is not incorrect.

2

(b) 4;

1

(c) (i) 14;

1

(ii) 36;

If (c)(i) incorrect accept [50 – (c)(i)]

1

(d) Different genes;

Different (DNA) base sequences;

2

[7]

M15. (a) GCAAUG; ;

Allow one mark if T instead of U, i.e. GCAATG

2

(b) (i) DNA is edited / introns present in DNA;

Allow reference to 'junk' or non-coding DNA

1

(ii) 220; allow 218 or 219-allow 2
Three bases / nucleotides code for one amino acid;
Correct explanation for 218 or 219;

2

(c) mRNA has no base-pairing, tRNA has base-pairing / mRNA linear, tRNA cloverleaf shape; mRNA has no binding site for amino acids, tRNA has; mRNA different for each gene / many kinds, only few / 20 / 64 kinds of tRNA; accept mRNA longer / larger / more nucleotides than tRNA

max 2

[7]

M16. (a) (i) ACG;

1

(ii) serine;

1

(b) idea that DNA contains introns / mRNA is only exons / mRNA is "edited';
(allow junk / non-sense DNA)

1

(c) binds to / blocks codon / triplet on mRNA so anticodon / tRNA will not fit in / base-pair;
amino acids not delivered / joined;

Accept translation will not occur for 1 mark

2

[5]

M17. (a) Protein made of (chain of) amino acids;
Each amino acid has its own base / triplet code;

2

(b) UCA = 2 marks
TCA – 1 mark;

2

(c) CCG;
GGG GGG;

2

(d) (i) Changes base sequence;
Of later triplets / amino acid codes;

2

(ii) S-phase / interphase;

1

(e)
1. mRNA leaves (nucleus) through nuclear pore;
2. To ribosome;
3. tRNA molecules bring amino acids (to ribosome);
4. Specific tRNA molecule for specific amino acid;
5. Anticodon of tRNA corresponds / complementary to codon on mRNA;
6. Peptide bonds form between amino acids;
7. tRNA detaches and collects another amino acid;
8. Ribosome moves along mRNA;

max 6

[15]

M18. (a) (i) C → B → E → F → A → D
Mark links: 5 correct = 2, 4 correct = 1, <4 correct = 0

2

(iii) nucleus;

1

(iii) A, D, F; *(ignore E if evident)*

1

(b) (i) Isoleucine;

1

(ii) TGG;

1

[6]

M19. (a) (i) join / attach nucleotides, to form a strand / along backbone /

phosphodiester bonds;

(reject reference to H bonds, complementary base pairing)

1

(ii) ribosome / RER;

1

(b) (i) CGTTACCAA;

1

(ii) CGU UAC CAA;

1

(c) substitution;

1

(d) (i) alanine;

1

(ii) (mutation 1)
no change(to sequence of amino acids);
codon for alanine / degenerate codon / same amino acid coded for;

2

(mutation 2)
(change in sequence) valine replaced by alanine / codon for alanine;
folding / shape / tertiary structure / position of bonds may change;

(reject peptide bonds)

2

[10]

M20. (a) AGC; TTC;

2

(b) anticodon complementary to codon / reads message on mRNA;
specific amino acid;
carried / transferred (to ribosome);
correct sequence of amino acids along polypeptide;

3 max

(c)

(Met)	Phe	Gln	Gln	Lys	Gln	Phe

2

(three / four / five correct 1 mark; six correct 2 marks)

[7]

M21. (a) high energy radiation / ionising particles;
named particles / α, β, γ;
colchicine;
x rays / cosmic rays;
uv (light);
carcinogen / named carcinogen;
mustard gas / phenols / tar (qualified);

1 max

(b) (i) removal of one or more bases / nucleotide;
frameshift / (from point of mutation) base sequence change;

2

(ii) sequence of bases in mRNA would change;
(sequence of) amino acids different / different primary structure;
(active site / enzyme 1) changed tertiary shape / changed active sites;
white pigment does not bind;
lilac pigment not produced / white pigment remains unchanged / enzyme 1 does not function;

4 max

(iii) blue and lilac; white;

colour of petal
(white)
blue
lilac;
white;

2

[9]

M22. (a) 387;

1

(b) (i) CCAG;

1

(ii) 5;

1

(c) high energy radiation / X rays / ultraviolet light / gamma rays;
high energy particles / alpha particles / beta particles;
named chemical mutagens e.g. benzene / caffeine / pesticide / mustard gas / tobacco tar / free radicals;
(two named examples of any of the above = 2 marks)
length of time of exposure (to a mutagen);
dosage (of mutagen);

2 max

(d) (i) UAC UUA UGG;

1

(ii) addition and deletion (of bases / nucleotides);
thymine added;
adenine deleted;
(addition of thymine and deletion of adenine = 3 marks)
(allow addition of adenine (RNA) and deletion of uracil (RNA) = 2 marks)

3

[9]

M23. (a) (i) number of bases = 4440
allow 4446 if they refer to start / stop

each amino acid coded for by triplet / three bases
(so three times more bases than amino acids);

2

(ii) deletion;
(deletion) of three bases;
because substitution / addition would change amino acid(s);

2 max

(b) (i) codon on mRNA;
specific / complementary base pairing with;
anti-codon on tRNA;

specific tRNA for each amino acid;
protein formed by condensation reactions /
peptide bonds formed;

4 max

(ii) (loss of amino acid) changes tertiary structures / 3D shape;
so sugar molecules cannot be attached (to form glycoprotein / functional protein);
so (defective) unable to bind to chloride ions / use ATP;

2 max

[10]